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Announcing the New
GeneChip® Rat Genome 230 2.0 Array


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**:: QUERY
Expression**
-> Quick Query
-> Standard Query
-> Batch Query
-> BLAST
-> Probe Match
-> UCSC Query

Genotyping
-> Quick Query
-> Standard Query
-> Batch Query
-> UCSC Query
-> SNP Finder

**:: CURRENT QUERY
1 probe sets**
-> Annotations
-> Show Orthologs
-> GO Browser
-> Export

:: QUERY HISTORY

Annotation Views
-> Expression
-> Genotyping

-> BLAST Status

-> New Folder

-> **Expression
Queries**
-> (1) All Descriptions
(AFFX-BioB-M_st)
-> (1) All Descriptions
(HG613)
-> (2) All Descriptions
(AFFX-BioDn-5)
-> (2) All Descriptions
(AFFX-BioB-M)
-> (1) All Descriptions
(M12625_at)

-> **Genotyping
Queries**

Full Record

Details for HUGENEFL:AFFX-BIOB-M_ST

Full Screen

NetAffx Links [Cluster Members](#)
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GeneChip Array Information

Probe Set ID AFFX-BioB-M_st
**GeneChip
Array** HumanGeneFL Array
**Organism
Common
Name** Human

Probe Design Information

Transcript ID AFFX-BioB-M
**Sequence
Type** Control sequence
**Representative
Public ID** J04423 [NCBI](#)
**Target
Description** J04423 E coli bioB gene biotin synthetase (-5, -M, -3 represent transcript regions
5 prime, Middle, and 3 prime respectively)

Sequence

**Target
Sequence**
>HUGENEFL:AFFX-BIOB-M_ST
gccggagttttacggcaatatcatcaccacacgcacttatcaggaacgcctcgatacgct
ggaaaaagtgcgcgatgccgggatcaaagtctgttctggcgccattgtgggcttaggcga
aacggtaaaagatcgccggattattgctgcaactggcaaacctgccgacgcgcgcgga
aagcgtgccaatcaacatgctggtgaaaggcacgcgcgttgccgataacgatga
tgtcgatgcctttgattt

	Probe Sequence(5'-3')	Probe		Probe Interrogation Position	Strandedness
		X	Y		
Probe Info	GATGATATTGCCGTA AAACTCCGGC	201	11	483	Sense
	TGTGGTGATGATATTGCCGTA AAAAC	202	11	489	Sense
	TAAGTGCGTGTGGTGATGATATTGC	203	11	497	Sense
	GTTCTGATAAGTGCGTGTGGTGAT	204	11	505	Sense
	ATCGAGGCGTTCCTGATAAGTGCGT	205	11	513	Sense
	GCATCGCGCACTTTTCCAGCGTAT	206	11	536	Sense
	GATCCCGGCATCGCGCACTTTTCC	207	11	543	Sense
	GACTTTGATCCCGGCATCGCGCACT	208	11	549	Sense
	CGCCAGAACAGACTTTGATCCCGGC	209	11	559	Sense
	CCCACAATGCCGCCAGAACAGACTT	210	11	569	Sense

TGCAGCAATAATCCGGCGCGATCTT	211	11	611	Sense
TTGCCAGTTGCAGCAATAATCCGGC	212	11	619	Sense
CGGCAGGTTTGCCAGTTGCAGCAAT	213	11	627	Sense
ATGTTGATTGGCACGCTTTCCGGCG	214	11	656	Sense
CACCAGCATGTTGATTGGCACGCTT	215	11	663	Sense
TTACCTTCACCAGCATGTTGATTG	216	11	671	Sense
AGCGGCGTGCCTTTCACCTTCACCA	217	11	683	Sense
CATCATCGTTATCGGCAAGCGGCGT	218	11	700	Sense
GCATCGACATCATCGTTATCGGCAA	219	11	707	Sense
AAATCAAAGGCATCGACATCATCGT	220	11	716	Sense

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